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(57) Abstract

Catalase enzymes derived from bacterial for the genera *Alcaligenes (Delaya)* and *MicroscUla* are disclosed. The enzymes are produced from native or recombinant host cells and can be utilized to destroy or detect hydrogen peroxide, e.g., in production of glyoxylic acid and in glucose sensors, and in processes where hydrogen peroxide is used as a bleaching or antibacterial agent, e.g., in contact lens cleaning, in bleaching steps in pulp and paper preparation and in the pasteurization of dairy products.

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CATALASES

Field of the Invention

This invention relates generally to enzymes and more specifically to catalases and polynucleotides encoded such catalases, including methods of use.

Background

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the production and isolation of such polynucleotides and polypeptides. More particularly, the polynucleotides and polypeptides of the present invention have been putatively identified as catalases.

Generally, in processes where hydrogen peroxide is a by-product, catalases can be used to destroy or detect hydrogen peroxide, *e.g.*, in production of glyoxylic acid and in glucose sensors. Also, in processes where hydrogen peroxide is used as a bleaching or antibacterial agent, catalases can be used to destroy residual hydrogen peroxide, *e.g.* in contact lens cleaning, in bleaching steps in pulp and paper preparation and in the pasteurization of dairy products. Further, such catalases can be used as catalysts for oxidation reactions, *e.g.*, epoxidation and hydroxylation.

Summary of the Invention

In accordance with one aspect of the present invention, there are provided novel enzymes, as well as active fragments, analogs and derivatives thereof.

In accordance with another aspect of the present invention, there are provided isolated nucleic acid molecules encoding the enzymes of the present invention including mRNAs, cDNAs, genomic DNAs as well as active analogs and fragments of such enzymes.

In accordance with yet a further aspect of the present invention, there is provided a process for producing such polypeptides by recombinant techniques comprising culturing recombinant prokaryotic and/or eukaryotic host cells, containing a nucleic acid sequence of the present invention, under conditions promoting expression of said enzymes and subsequent recovery of said enzymes.

In accordance with yet a further aspect of the present invention, there are also provided nucleic acid probes comprising nucleic acid molecules of sufficient length to specifically hybridize to a nucleic acid sequence of the present invention.

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such enzymes, or polynucleotides encoding such enzymes, for *in vitro* purposes related to scientific research, for example, to generate probes for identifying similar sequences which might encode similar enzymes from other organisms by using certain regions, i.e., conserved sequence regions, of the nucleotide sequence.

In accordance with yet a further aspect of the present invention, there is provided antibodies to such catalases. These antibodies are as probes to screen libraries from these or other organisms for members of the libraries which could have the same catalase activity or a cross reactive activity.

In another embodiment, the invention provides a method for catalyzing an oxidation reaction comprising contacting a substrate with an effective amount of an enyzme selected from the group consisting of an amino acid sequence set forth in SEQ ID NOS: 7 or 9, thereby catalyzing an oxidation reaction. Another method of the invention includes the detection and/or destruction of hydrogen peroxide in a

sample comprising contacting the sample with an effective amount of an enzyme having an amino acid sequence set forth in SEQ ID NO:7 or SEQ ID NO:9, and detecting the presence of hydrogen peroxide in the sample. Hydrogen peroxide acts as a substrate for catalases, thus, either the detection and/or the destruction of hydrogen peroxide is achieved by combining a sufficient amount of the catalases of the invention with a sample or material suspected of containing hydrogen peroxide.

These and other aspects of the present invention should be apparent to those skilled in the art from the teachings herein.

Brief Description of the Drawings

The following drawings are illustrative of an embodiment of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

Figure 1 shows the full-length DNA sequence and the corresponding deduced amino acid sequence for *Alcaligenes (Deleya) aquamarinus* Catalase - 64CA2.

Figure 2 shows the full-length DNA sequence and the corresponding deduced amino acid sequence for *Microscilla furvescens* Catalase 53CA 1.

Detailed Description of Preferred Embodiments

In order to facilitate understanding of the following description and examples which follow certain frequently occurring methods and/or terms will be described.

The term "isolated" means altered "by the hand of man" from its natural state; i.e., if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring polynucleotide or a polypeptide naturally present in a living animal in its natural state is not "isolated", but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. For example, with respect to polynucleotides, the term isolated means that it is separated from the nucleic acid and cell in which it naturally occurs.

As part of or following isolation, such polynucleotides can be joined to other polynucleotides, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated polynucleotides, alone or joined to other polynucleotides such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such polynucleotides still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the polynucleotides and polypeptides may occur in a composition, such as a media formulation (solutions for introduction of polynucleotides or polypeptides, for example, into cells or compositions or solutions for chemical or enzymatic reactions which are not naturally occurring compositions) and, therein remain isolated polynucleotides or polypeptides within the meaning of that term as it is employed herein.

The term "ligation" refers to the process of forming phosphodiester bonds between two or more polynucleotides, which most often are double stranded DNAs. Techniques for ligation are well known to the art and protocols for ligation are described in standard laboratory manuals and references, such as, for instance, Sambrook et al., MOLECULAR CLONING, A LABORATORY MANUAL, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989).

The term "gene" means the segment of DNA involved in 4producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as intervening sequences (introns) between individual coding segments (exons).

A coding sequence is "operably linked to" another coding sequence when RNA polymerase will transcribe the two coding sequences into a single mRNA, which is then translated into a single polypeptide having amino acids derived from both coding sequences. The coding sequences need not be contiguous to one another so long as the expressed sequences ultimately process to produce the desired protein.

"Recombinant" enzymes refer to enzymes produced by recombinant DNA techniques; i.e., produced from cells transformed by an exogenous DNA construct

encoding the desired enzyme. nSynthetic" enzymes are those prepared by chemical synthesis.

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular enzyme, is a DNA sequence which is transcribed and translated into an enzyme when placed under the control of appropriate regulatory sequences.

"Plasmids" are designated by a lower case "p" preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes

used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 μg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 μl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 μg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37.C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel et al., *Nucleic Acids Res.*, *8*:4057 (1980).

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the

presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., et al., Id., p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units of T4 DNA ligase ("ligase") per 0.5 μg of approximately equimolar amounts of the DNA fragments to be ligated.

Unless otherwise stated, transformation was performed as described in Sambrook and Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1989.

In accordance with an aspect of the present invention, there are provided isolated nucleic acids (polynucleotides) which encode for the mature enzyme having the deduced amino acid sequence of Figure 1 (SEQ ID NO: 7).

In accordance with another aspect of the present invention, there are provided isolated nucleic acids (polynucleotides) which encode for the mature enzyme having the deduced amino acid sequence of Figure 2 (SEQ ID NO: 9).

In accordance with another aspect of the present invention, there is provided an isolated polynucleotide encoding the enzyme of the present invention. The deposited material is a genomic clone comprising DNA encoding an enzyme of the present invention. As deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, USA, the deposited material is assigned ATCC Deposit No.

The deposit has been made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for Purposes of Patent Procedure. The clone will be irrevocably (without restriction or condition) released to the public upon the issuance of a patent. This deposit is provided merely as convenience to those of skill in the art and is not an admission that a deposit would be required under 35 U.S.C. §112. The sequence of the polynucleotide contained in the deposited material, as well as the amino acid sequence of the polypeptide encoded thereby, are controlling in the event of any conflict with any description of sequences

herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The polynucleotides of this invention were originally recovered from a genomic gene library derived from two sources. The first, *Alcaligenes (Delaya) aquamarinus*, is a β-Proteobacteria. It is a gram-negative rod that grows optimally at 26° C and pH 7.2. The second, *Microscilla furvescens*, is a Cytophagales (Bacteria) isolated from Samoa. It is a gram-negative rod with gliding motility that grows optimally at 30° C and pH 7.0.

With respect to *Alcaligenes (Delaya) aquamarinus*, the protein with the closest amino acid sequence identity of which the inventors are currently aware is the *Microscilla furvescens* catalase (59.5 % protein identity; 60 % DNA identity). The next closest is a *Mycobacterium tuberculosis* catalase (KatG), with a 54 % protein identity.

With respect to *Microscilla furvescens*, the protein with the closest amino acid sequence identity of which the inventors are currently aware is catalase I of *Bacillus stearothermophilas*, which has a 69% amino acid identity.

Accordingly, the polyoucleotides and enzymes encoded thereby are identified by the organism from which they were isolated. Such are sometimes referred to below as "64CA2" (Figure 1 and SEQ ID NOS: 6 and 7) and "53CA1" (Figure 2 and SEQ ID NOS: 8 and 9).

One means for isolating the nucleic acid molecules encoding the enzymes of the present invention is to probe a gene library with a natural or artificially designed probe using art recognized procedures (see, for example: Current Protocols in Molecular Biology, Ausubel F.M. *et al.* (EDS.) Green Publishing Company Assoc. and John Wiley Interscience, New York, 1989, 1992). It is appreciated by one skilled in the art that the polynucleotides of SEQ ID NOS: 6 and 8, or fragments thereof (comprising at least 12 contiguous nucleotides), are particularly useful probes. Other particularly useful probes for this purpose are hybridizable fragments of the sequences of SEQ ID NOS: 6 and 8 (i.e., comprising at least 12 contiguous nucleotides).

With respect to nucleic acid sequences which hybridize to specific nucleic acid sequences disclosed herein, hybridization may be carried out under conditions of reduced stringency, medium stringency or even stringent conditions. As an example of oligonucleotide hybridization, a polymer membrane containing immobilized denatured nucleic acids is first prehybridized for 30 minutes at 45°C in a solution consisting of 0.9 M NaCl, 5.0 mM NaH_2PO_4, pH 7.0, 5.0 mM Na_2EDTA, 0.5% SDS, 10X Denhardt's, and 0.5 mg/mL polyriboadenylic acid. Approximately 2 X 10^7 cpm (specific activity 4-9 X 10^8 cpm/ug) of ^{32}p end-labeled oligonucleotide probe are then added to the solution. After 1216 hours of incubation, the membrane is washed for 30 minutes at room temperature in 1X SET (150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na_2EDTA) containing 0.5% SDS, followed by a 30 minute wash in fresh 1X SET at (Tm less 10°C) for the oligonucleotide probe. The membrane is then exposed to auto-radiographic film for detection of hybridization signals.

Stringent conditions means hybridization will occur only if there is at least 90% identity, preferably at least 95 % identity and most preferably at least 97% identity between the sequences. Further, it is understood that a section of a lOO bps sequence that is 95 bps in length has 95% identity with the 1090 bps sequence from which it is obtained. See J. Sambrook *et al., Molecular Cloning, A Laboratory Manual, 2d Ed.*, Cold Spring Harbor Laboratory (1989) which is hereby incorporated by reference in its entirety. Also, it is understood that a fragment of a 100 bps sequence that is 95 bps in length has 95% identity with the 100 bps sequence from which it is obtained.

As used herein, a first DNA (RNA) sequence is at least 70% and preferably at least 80% identical to another DNA (RNA) sequence if there is at least 70% and preferably at least a 80% or 90% identity, respectively, between the bases of the first sequence and the bases of the another sequence, when properly aligned with each other, for example when aligned by BLASTN.

The present invention relates to polynucleotides which differ from the reference polynucleotide such that the differences are silent, for example, the amino acid sequence encoded by the polynucleotides is the same. The present invention also

relates to nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference polynucleotide. In a preferred aspect of the invention these polypeptides retain the same biological action as the polypeptide encoded by the reference polynucleotide.

The polynucleotides of this invention were recovered from genomic gene libraries from the organisms identified above. Gene libraries were generated from a Lambda ZAP II cloning vector (Stratagene Cloning Systems). Mass excisions were performed on these libraries to generate libraries in the pBluescript phagemid. Libraries were generated and excisions were performed according to the protocols/methods hereinafter described.

The polynucleotides of the present invention may be in the form of RNA or DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequences which encodes the mature enzymes may be identical to the coding sequences shown in Figures 1-2 (SEQ ID NOS: 6 & 8) or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same mature enzymes as the DNA of Figures 12 (SEQ ID NOS: 6 & 8).

The polynucleotide which encodes for the mature enzyme of Figures 1-2 (SEQ ID NOS: 7 & 9) may include, but is not limited to: only the coding sequence for the mature enzyme; the coding sequence for the mature enzyme and additional coding sequence such as a leader sequence or a proprotein sequence; the coding sequence for the mature enzyme (and optionally additional coding sequence) and non-coding sequence, such as introns or noncoding sequence 5' and/or 3' of the coding sequence for the mature enzyme.

Thus, the term "polynucleotide encoding an enzyme (protein)" encompasses a polynucleotide which includes only coding sequence for the enzyme as well as a polynucleotide which includes additional coding and/or non-coding sequence.

The present invention further relates to variants of the hereinabove described polynucleotides which encode for fragments, analogs and derivatives of the enzymes having the deduced amino acid sequences of Figures 1-2 (SEQ ID NOS: 7 & 9). The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a nonnaturally occurring variant of the polyoucleotide.

Thus, the present invention includes polynucleotides encoding the same mature enzymes as shown in Figures 1-2 (SEQ ID NOS: 7 & 9) as well as variants of such polynucleotides which variants encode for a fragment, derivative or analog of the enzymes of Figures 1-2 (SEQ ID NOS: 7 & 9). Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

As hereinabove indicated, the polynucleotides may have a coding sequence which is a naturally occurring allelic variant of the coding sequences shown in Figures 1-2 (SEQ ID NOS: 6 & 8). As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded enzyme. Also, using directed and other evolution strategies, one may make very minor changes in DNA sequence which can result in major changes in function.

Fragments of the full length gene of the present invention may be used as hybridization probes for a cDNA or a genomic library to isolate the full length DNA and to isolate other DNAs which have a high sequence similarity to the gene or similar biological activity. Probes of this type preferably have at least 10, preferably at least 15, and even more preferably at least 30 bases and may contain, for example, at least 50 or more bases. In fact, probes of this type having at least up to 150 bases or greater may be preferably utilized. The probe may also be used to identify a DNA clone corresponding to a full length transcript and a genomic clone or clones that contain the complete gene including regulatory and promotor regions, exons and introns. An example of a screen comprises isolating the coding region of the gene by using the known DNA sequence to synthesize an oligonucleotide probe. Labeled oligonucleotides having a sequence complementary or identical to that of the gene or

portion of the gene sequences of the present invention are used to screen a library of genomic DNA to determine which members of the library the probe hybridizes to.

It is also appreciated that such probes can be and are preferably labeled with an analytically detectable reagent to facilitate identification of the probe. Useful reagents include but are not limited to radioactivity, fluorescent dyes or enzymes capable of catalyzing the formation of a detectable product. The probes are thus useful to isolate complementary copies of DNA from other sources or to screen such sources for related sequences.

The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 70%, preferably at least 90%, and more preferably at least 95% identity between the sequences. (As indicated above, 70% identity would include within such definition a 70 bps fragment taken from a 100 bp polynucleotide, for example.) The present invention particularly relates to polynucleotides which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95 % and preferably at least 97% identity between the sequences. The polyoucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode enzymes which either retain substantially the same biological function or activity as the mature enzyme encoded by the DNA of Figures 1-2 (SEQ ID NOS: 6 & 8). In referring to identity in the case of hybridization, as known in the art, such identity refers to the complementarily of two polynucleotide segments.

Alternatively, the polynucleotide may have at least 15 bases, preferably at least 30 bases, and more preferably at least 50 bases which hybridize to any part of a polynucleotide of the present invention and which has an identity thereto, as hereinabove described, and which may or may not retain activity. For example, such polynucleotides may be employed as probes for the polynucleotides of SEQ ID NOS: 6 & 8, for example, for recovery of the polyoucleotide or as a diagnostic probe or as a PCR primer.

Thus, the present invention is directed to polynucleotides having at least a 70% identity, preferably at least 90% identity and more preferably at least a 95% identity to a polynucleotide which encodes the enzymes of SEQ ID NOS: 7 & 9 as well as fragments thereof, which fragments have at least 15 bases, preferably at least 30 bases, more preferably at least 50 bases and most preferably fragments having up to at least 150 bases or greater, which fragments are at least 90% identical, preferably at least 95% identical and most preferably at least 97% identical to any portion of a polynucleotide of the present invention.

The present invention further relates to enzymes which have the deduced amino acid sequences of Figures 1-9 (SEQ ID NOS: 28-36) as well as fragments, analogs and derivatives of such enzyme.

The terms "fragment,n nderivative" and "analog" when referring to the enzymes of Figures 1-9 (SEQ ID NOS. 28-36) means enzymes which retain essentially the same biological function or activity as such enzymes. Thus, an analog includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature enzyme.

The enzymes of the present invention may be a recombinant enzyme, a natural enzyme or a synthetic enzyme, preferably a recombinant enzyme.

The fragment, derivative or analog of the enzymes of Figures 1-2 (SEQ ID NOS: 7 & 9) may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the mature enzyme is fused with another compound, such as a compound to increase the half-life of the enzyme (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the mature enzyme, such as a leader or secretory sequence or a sequence which is employed for purification of the mature enzyme or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

The enzymes and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of enzymes of the invention by recombinant techniques.

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector such as an expression vector. The vector may be, for example, in the form of a plasmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the present invention. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The polynucleotides of the present invention may be employed for producing enzymes by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing an enzyme. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, *e.g.*, derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli. lac* or *trp,* the phage lambda P_L promoter and other promoters

known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli, Streptomyces, Bacillus subtilis*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; plant cells, *etc*. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example; Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBluescript II KS(Stratagene), ptrc99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene) pSVK3, pBPV, pMSG, pSVL SV40 (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

Promoter regions can be selected from any desired gene using CAT

(chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, apt, lambda PR, PL and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis, L., Dibner, M., Battey, I., *Basic Methods in Molecular Biology,* (1986).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the enzymes of the invention can be synthetically produced by conventional peptide synthesizers.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, Second Edition*, Cold Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Transcription of the DNA encoding the enzymes of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cisacting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and

adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highlyexpressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated enzyme. Optionally, the heterologous sequence can encode a fusion enzyme including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli, Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host

strain to an appropriate cell density, the selected promoter is induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell, 23*: 175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

The enzyme can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, afflnity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing confi~uration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The enzymes of the present invention may be a naturally purified product, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast,

higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the enzymes of the present invention may be glycosylated or may be non-glycosylated. Enzymes of the invention may or may not also include an initial methionine amino acid residue.

Antibodies generated against the enzymes corresponding to a sequence of the present invention can be obtained by direct injection of the enzymes into an animal or by administering the enzymes to an animal, preferably a nonhuman. The antibody so obtained will then bind the enzymes itself. In this manner, even a sequence encoding only a fragment of the enzymes can be used to generate antibodies binding the whole native enzymes. Such antibodies can then be used to isolate the enzyme from cells expressing that enzyme.

The term "antibody," as used herein, refers to intact immunoglobulin molecules, as well as fragments of immunoglobulin molecules, such as Fab, Fab', $(Fab')_2$, Fv, and SCA fragments, that are capable of binding to an epitope of an endoglucanase polypeptide. These antibody fragments, which retain some ability to selectively bind to the antigen (*e.g.*, an endoglucanase antigen) of the antibody from which they are derived, can be made using well known methods in the art (see, *e.g.*, Harlow and Lane, *supra*), and are described further, as follows.

(1) A Fab fragment consists of a monovalent antigen-binding fragment of an antibody molecule, and can be produced by digestion of a whole antibody molecule with the enzyme papain, to yield a fragment consisting of an intact light chain and a portion of a heavy chain.

(2) A Fab' fragment of an antibody molecule can be obtained by treating a whole antibody molecule with pepsin, followed by reduction, to yield a molecule consisting of an intact light chain and a portion of a heavy chain. Two Fab' fragments are obtained per antibody molecule treated in this manner.

(3) A $(Fab')_2$ fragment of an antibody can be obtained by treating a whole antibody molecule with the enzyme pepsin, without subsequent reduction. A $(Fab')_2$ fragment is a dimer of two Fab' fragments, held together by two disulfide bonds.

(4) An Fv fragment is defined as a genetically engineered fragment containing the variable region of a light chain and the variable region of a heavy chain expressed as two chains.

(5) A single chain antibody ("SCA") is a genetically engineered single chain molecule containing the variable region of a light chain and the variable region of a heavy chain, linked by a suitable, flexible polypeptide linker.

As used in this invention, the term "epitope" refers to an antigenic determinant on an antigen, such as an endoglucanase polypeptide, to which the paratope of an antibody, such as an endoglucanase-specific antibody, binds. Antigenic determinants usually consist of chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three-dimensional structural characteristics, as well as specific charge characteristics.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497, 1975), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72, 1983), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96, 1985).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic enzyme products of this invention. Also, transgenic mice may be used to express humanized antibodies to immunogenic enzyme products of this invention.

Antibodies generated against an enzyme of the present invention may be used in screening for similar enzymes from other organisms and samples. Such screening techniques are known in the art, for example, one such screening assay is described in Sambrook and Maniatis, Molecular Cloning: A Laboratory Manual (2d Ed.), vol. 2:Section 8.49, Cold Spring Harbor Laboratory, 1989, which is hereby incorporated by reference in its entirety.

The present invention will be further described with reference to the following examples; however, it is to be understood that the present invention is not limited to such examples. All parts or amounts, unless otherwise specified, are by weight.

Example 1

Production of the Expression Gene Bank

An *E. coli* catalase negative host strain CAT500 was infected with a phage solution containing sheared pieces of DNA from *Alcaligenes (Deleya) aquamarinus* in pBluescript plasmid and plated on agar containing LB with ampicillin (100 ~g/mL), methicillin (80 ~g/mL) and kanamycin (100 ~g/mL) according to the method of Hay and Short (Hay, B. and Short, J., *J. Strategies*, 5:16, 1992). The resulting colonies were picked with sterile toothpicks and used to singly inoculate each of the wells of 96-well microtiter plates. The wells contained 250 ,uL of SOB media with 100 ~g/mL ampicillin, 80 ~g/mL methicillin, and (SOB Amp/Meth/Kan). The cells were grown overnight at 37°C without shaking. This constituted generation of the "SourceGeneBankn; each well of the Source GeneBank thus contained a stock culture of *E. coli* cells, each of which contained a pBluescript plasmid with a unique DNA insert. Same protocol was adapted for screening catalase from *Microscilla furvescens*.

Example 2

Screening for Catalase Activity

The plates of the Source GeneBank were used to multiply inoculate a single plate (the "Condensed Plate") containing in each well 200 μL of SOB Amp/Meth/Kan. This step was performed using the High Density Replicating Tool (HDRT) of the Beckman Biomek with a 1 % bleach, water, isopropanol, air-dry sterilization cycle in between each inoculation. Each well of the Condensed Plate thus contained 4 different

pBluescript clones from each of the source library plates. Nine such condensed plates were prepared and grown for 16h at 37°C.

One hundred (100) µL of the overnight culture was transferred to the white polyfiltronic assay plates containing 100 µL Hepes/well. A 0.03% solution of hydrogen peroxide was made in 5 % Triton and 20 µL of this solution was added to each well. The plates were incubated at room temperature for one hour. After an hour, 50 ,µL of 120 mM 3-(p-hydroxyphenyl)-propionic acid and 1 unit of horseradish peroxidase were added to each well and the plates were incubated at room temperature for 1 hour. To quench the reaction, 50 ,µL of 1 M Tris-base was added to each wel1. The wells were excited on a fluorometer at 320 nm and read at 404 nm. A low value signified a positive catalase hit.

Example 3

Isolation and Purification of the Active Clone

In order to isolate the individual clone which carried the activity, the Source GeneBank plates were thawed and the individual wells used to singly inoculate a new plate containing SOB Amp/Meth/Kan. As above the plate was incubated at 37°C to grow the cells, and assayed for activity as described above. Once the active well from the source plate was identified, the cells from the source plate were streaked on agar with LB/Amp/Meth/Kan and grown overnight at 37°C to obtain single colonies. Eight single colonies were picked with a sterile toothpick and used to singly inoculate the wells of a 96well microtiter plate. The wells contained 250 pL of SOB Amp/Meth/Kan. The cells were grown overnight at 37°C without shaking. A 100 µL aliquot was removed from each well and assayed as indicated above. The most active clone was identified and the remaining 150 µL of culture was used to streak an agar plate with LB/Amp/Meth/Kan. Eight single colonies were picked, grown and assayed as above. The most active clone was used to inoculate 3mL cultures of LB/Amp/Meth/Kan, which were grown overnight. The plasmid DNA was isolated from the cultures and utilized for sequencing.

Example 4

Expression of Catalases

DNA encoding the enzymes of the present invention, SEQ ID NOS: 7 and 9, were initially amplified from a pBluescript vector containing the DNA by the PCR technique using the primers noted herein. The amplified sequences were then inserted into the respective pQE vector listed beneath the primer sequences, and the enzyme was expressed according to the protocols set forth herein. The 5' and 3' oligonucleotide primer sequences used for subcloning and vectors for the respective genes are as follows:

Alcaligenes (Deleya) aquamarinus catalse: (pQET vector)

5' Primer

CCGAGAATTCATTAAAGAGGAGAAATTAACTATGAATAACGCATCCGCTGAC EcoRI (SEQ ID NO:1)

3 ' Primer CGGAAAGCTTTTACGACGCGACGTCGAAACG HindI I I (SEQ ID NO:2)

Microscilla furvescens catalase: (pQET vector)

5' Primer

CCGAGAATTCATTAAAGAGGAGAAATTAACTATGGAAAATCACAAACACTCA EcoRI (SEQ ID NO:3)

3' Primer CGAAGGTACCTTATTTCAGATCAAACCGGTC Kpnl (SEQ ID NO:4)

The restriction enzyme sites indicated correspond to the restriction enzyme sites on the bacterial expression vector indicated for the respective gene (Qiagen, Inc. Chatsworth, CA). The pQET vector encodes antibiotic resistance (Ampr), a bacterial origin of replication (ori), an IPTG-regulatable promoter operator (P/O), a ribosome binding site (RBS), a 6-His tag and restriction enzyme sites.

The pQET vector was digested with the restriction enzymes indicated. The amplified sequences were ligated into the respective pQET vector and inserted in

frame with the sequence encoding for the RBS. The native stop codon was incorporated so the genes were not fused to the His tag of the vector. The ligation mixture was then used to transform the E. cold strain UM255tpREP4 (Qiagen, Inc.) by electroporation. UM255/pREP4 contains multiple copies of the plasmid pREP4, which expresses the lacl repressor and also confers kanamycin resistance (Kanr). Transformants were identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies were selected. Plasmid DNA was isolated and confirmed by restriction analysis. Clones containing the desired constructs were grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 u μ/ml) and Kan (25 u μ/ml). The O/N culture was used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells were grown to an optical density 600 (O.D.^{600}) of between 0.4 and 0.6. IPTG ("Isopropyl-B-D-thiogalacto pyranosiden") was then added to a final concentration of 1 mM. IPTG induces by inactivating the lacl repressor, clearing the P/O leading to increased gene expression. Cells were grown an extra 3 to 4 hours. Cells were then harvested by centrifugation. The primer sequences set out above may also be employed to isolate the target gene from the deposited material by hybridization techniques described above.

Cited Literature

1) Patent 5, 439,813, Aug. 8, 1995, Production of glyoxylic acid with glycolate oxidase and catalase immobilized on oxirane acrylic beads, Anton, D. L., Wilmington, DE, DiCosimo, R., Wilmington, DE, Gavagan, I.E., Wilmington, DE.

2) Patent: 5,360,732, Nov.1, 1994, Production of Aspergillus niger catalase-R, Berka, R. M., San Mateo, CA, Fowler, T., Redwood City, CA, Rey, M.W., San Mateo, CA.

3) Patent: 4,460,686, 1ul. 17, 1984, Glucose oxidation with immobilized glucose oxidasecatalase, Hartmeier, W., Ingelheim am Rhein, Germany

4) Patent: 5,447,650, Sep. 5, 1995, Composition for preventing the accumulation of inorganic deposits on contact lenses, Cafaro, D.P., Santa Ana, CA

5) Patent: 5,362,647, Nov. 8, 1994, Compositions and methods for destroying hydrogen peroxide, Cook, I.N., Mission Viejo, CA, Worsley, I.L., Irvine, CA.

6) Patent: 5,266,338, 1993, Cascione, A.S., Rapp, H.

7) Patrick Dhaese, "Catalase: An Enzyme with Growing Industrial Potential~ CHIMICA OGGIA/Chemistry Today, Jan/Feb, 1996.

What Is Claimed Is:

1. Substantially pure catalase having an amino acid sequence of SEQ ID NO:7 or SEQ ID NO:9

2. An isolated polynucleotide sequence encoding a catalase of claim 1.

3. An isolated polynucleotide selected from the group consisting of:
   a) SEQ ID:6 or SEQ ID NO:8;
   b) SEQ ID:6 or SEQ ID NO:8, wherein T can also be U;
   c) nucleic acid sequences complementary to a) and b); and
   d) fragments of a), b), or c) that are at least 15 bases in length and that will selectively hybridize to DNA which encodes the amino acid sequences of SEQ ID Nos:7 or 9, respectively.

4. The polynucleotide of claim 2, wherein the polynucleotide is isolated from a prokaryote.

5. An expression vector including the polynucleotide of claim 2.

6. The vector of claim 5, wherein the vector is a plasmid.

7. The vector of claim 5, wherein the vector is a virus-derived.

8. A host cell transformed with the vector of claim 5.

9. The host cell of claim 8, wherein the cell is prokaryotic.

10. Antibodies that bind to the polypeptide of claim 1.

11. The antibodies of claim 10, wherein the antibodies are polyclonal.

12. The antibodies of claim 10, wherein the antibodies are monoclonal.

13. An enzyme comprising a member selected from the group consisting of:
   a) an enzyme comprising an amino acid sequence which is at least 70% identical to the amino acid sequence set forth in SEQ ID NO:7 or SEQ ID NO:9; and
   b) an enzyme which comprises at least 30 amino acid residues to an enzyme of a).

14. A method for producing an enzyme comprising growing a host cell of claim 8 under conditions which allow the expression of the nucleic acid and isolating the enzyme encoded by the nucleic acid.

15. A process for producing a cell comprising: transforming or transfecting the cell with the vector of Claim 5 such that the cell expresses the polypeptide encoded by the DNA contained in the vector.

16. A method for catalyzing an oxidation reaction comprising contacting a substrate with an effective amount of an enyzme selected from the group consisting of an amino acid sequence set forth in SEQ ID NOS: 7 or 9, thereby catalyzing an oxidation reaction.

17. A method for detection or destruction of hydrogen peroxide in a sample comprising contacting the sample with an effective amount of an enzyme having an amino acid sequence set forth in SEQ ID NO:7 or SEQ ID NO:9, and detecting
the presence of hydrogen peroxide in the sample.

FIGURE 1

Alcaligenes (Deleya) aquamarinus Catalase - 64CA2

1	ATG AAT AAC GCA TCC GCT GAC GAT CTA CAC AGT AGC TTG CAG CAA AGA TGC AGA GCA TTT	60
1	Met Asn Asn Ala Ser Ala Asp Asp Leu His Ser Ser Leu Gln Gln Arg Cys Arg Ala Phe	20
61	GTT CCC TTG GTA TCG CCA AGG CAT AGA GCA ATA AGG GAG AGA GCT ATG AGC GGT AAA TGT	120
21	Val Pro Leu Val Ser Pro Arg His Arg Ala Ile Arg Glu Arg Ala Met Ser Gly Lys Cys	40
121	CCT GTC ATG CAC GGT GGT AAC ACC TCG ACC GGT ACT TCC AAC AAA GAT TGG TGG CCG GAA	180
41	Pro Val Met His Gly Gly Asn Thr Ser Thr Gly Thr Ser Asn Lys Asp Trp Trp Pro Glu	60
181	GGG TTG AAC CTG GAT ATT TTG CAT CAG CAA GAT CGC AAA TCA GAC CCG ATG GAT CCG GAT	240
61	Gly Leu Asn Leu Asp Ile Leu His Gln Gln Asp Arg Lys Ser Asp Pro Met Asp Pro Asp	80
241	TTC AAC TAC CGT GAA GAA GTA CGC AAG CTC GAT TTC GAC GCG CTG AAG AAA GAT GTC CAC	300
81	Phe Asn Tyr Arg Glu Glu Val Arg Lys Leu Asp Phe Asp Ala Leu Lys Lys Asp Val His	100
301	GCG TTG ATG ACC GAT AGC CAA GAG TGG TGG CCC GCT GAC TGG GGG CAC TAC GGC GGT TTG	360
101	Ala Leu Met Thr Asp Ser Gln Glu Trp Trp Pro Ala Asp Trp Gly His Tyr Gly Gly Leu	120
361	ATG ATC CGT ATG GCT TGG CAC TCC GCT GGC ACC TAC CGT ATT GCT GAT GGC CGT GGG GGC	420
121	Met Ile Arg Met Ala Trp His Ser Ala Gly Thr Tyr Arg Ile Ala Asp Gly Arg Gly Gly	140
421	GGT GGT ACC GGA AGC CAG CGC TTT GCA CCG CTC AAC TCC TGG CCG GAC AAC GTC AGC CTG	480
141	Gly Gly Thr Gly Ser Gln Arg Phe Ala Pro Leu Asn Ser Trp Pro Asp Asn Val Ser Leu	160
481	GAT AAA GCG CGC CGT CTG CTG TGG CCG ATC AAG AAG AAG TAC GGC AAC AAA ATC AGC TGG	540
161	Asp Lys Ala Arg Arg Leu Leu Trp Pro Ile Lys Lys Lys Tyr Gly Asn Lys Ile Ser Trp	180
541	GCA GAC CTG ATG ATT CTG GCT GGC ACC GTG GCT TAT GAG TCC ATG GGC TTA CCT GCT TAC	600
181	Ala Asp Leu Met Ile Leu Ala Gly Thr Val Ala Tyr Glu Ser Met Gly Leu Pro Ala Tyr	200
601	GGC TTC TCT TTC GGC CGC GTC GAT ATT TGG GAA CCC GAA AAA GAT ATC TAC TGG GGT GAC	660
201	Gly Phe Ser Phe Gly Arg Val Asp Ile Trp Glu Pro Glu Lys Asp Ile Tyr Trp Gly Asp	220
661	GAA AAA GAG TGG CTG GCA CCT TCT GAC GAA CGC TAC GGC GAC GTG AAC AAG CCA GAG ACC	720
221	Glu Lys Glu Trp Leu Ala Pro Ser Asp Glu Arg Tyr Gly Asp Val Asn Lys Pro Glu Thr	240
721	ATG GAA AAC CCG CTG GCG GCT GTC CAA ATG GGT CTG ATC TAT GTG AAC CCG GAA GGT GTT	780
241	Met Glu Asn Pro Leu Ala Ala Val Gln Met Gly Leu Ile Tyr Val Asn Pro Glu Gly Val	260
781	AAC GGC CAC CCT GAT CCG CTG AGA ACC GCA CAG CAG GTA CTT GAA ACC TTC GCC CGT ATG	840
261	Asn Gly His Pro Asp Pro Leu Arg Thr Ala Gln Gln Val Leu Glu Thr Phe Ala Arg Met	280
841	GCG ATG AAC GAC GAA AAA ACC GCA GCC CTC ACA GCT GGC GGC CAC ACC GTC GGT AAT TGT	900
281	Ala Met Asn Asp Glu Lys Thr Ala Ala Leu Thr Ala Gly Gly His Thr Val Gly Asn Cys	300
901	CAC GGT AAT GGC AAT GCC TCT GCG TTA GCC CCT GAC CCA AAA GCC TCT GAC GTT GAA AAC	960
301	His Gly Asn Gly Asn Ala Ser Ala Leu Ala Pro Asp Pro Lys Ala Ser Asp Val Glu Asn	320
961	CAG GGC TTA GGT TGG GGC AAC CCC AAC ATG CAG GGC AAG GCA AGC AAC GCC GTG ACC TCG	1020
321	Gln Gly Leu Gly Trp Gly Asn Pro Asn Met Gln Gly Lys Ala Ser Asn Ala Val Thr Ser	340
1021	GGT ATC GAA GGT GCT TGG ACC ACC AAC CCC ACG AAA TTC GAT ATG GGC TAT TTC GAC CTG	1080
341	Gly Ile Glu Gly Ala Trp Thr Thr Asn Pro Thr Lys Phe Asp Met Gly Tyr Phe Asp Leu	360

1081 CTG TTC GGC TAC AAT TGG GAA CTG AAA AAG AGT CCT GCC GGT GCC CAC CAT TGG GAA CCG 1140
361 Leu Phe Gly Tyr Asn Trp Glu Leu Lys Lys Ser Pro Ala Gly Ala His His Trp Glu Pro 380

1141 ATT GAC ATC AAA AAG GAA AAC AAG CCG GTT GAC GCC AGC GAC CCC TCT ATT CGC CAC AAC 1200
381 Ile Asp Ile Lys Lys Glu Asn Lys Pro Val Asp Ala Ser Asp Pro Ser Ile Arg His Asn 400

1201 CCG ATC ATG ACC GAT GCG GAT ATG GCG ATA AAG GTA AAT CCG ACC TAT CGC GCT ATC TGC 1260
401 Pro Ile Met Thr Asp Ala Asp Met Ala Ile Lys Val Asn Pro Thr Tyr Arg Ala Ile Cys 420

1261 GAA AAA TTC ATG GCC GAT CCT GAG TAC TTC AAG AAA ACT TTC GCG AAG GCG TGG TTC AAG 1320
421 Glu Lys Phe Met Ala Asp Pro Glu Tyr Phe Lys Lys Thr Phe Ala Lys Ala Trp Phe Lys 440

1321 CTG ACG CAC CGT GAC CTG GGC CCG AAA TCA CGT TAC ATC GGC CCG GAA GTG CCG GCA GAA 1380
441 Leu Thr His Arg Asp Leu Gly Pro Lys Ser Arg Tyr Ile Gly Pro Glu Val Pro Ala Glu 460

1381 GAC CTG ATT TGG CAA GAC CCG ATT CCG GCA GGT AAC ACC GAC TAC TGC GAA GAA GTG GTC 1440
461 Asp Leu Ile Trp Gln Asp Pro Ile Pro Ala Gly Asn Thr Asp Tyr Cys Glu Glu Val Val 480

1441 AAG CAG AAA ATT GCA CAA AGT GGC CTG AGC ATT AGT GAG ATG GTC TCC ACC GCT TGG GAC 1500
481 Lys Gln Lys Ile Ala Gln Ser Gly Leu Ser Ile Ser Glu Met Val Ser Thr Ala Trp Asp 500

1501 AGT GCC CGT ACT TAT CGC GGT TCC GAT ATG CGC GGC GGT GCT AAC GGT GCC CGC ATT CGC 1560
501 Ser Ala Arg Thr Tyr Arg Gly Ser Asp Met Arg Gly Gly Ala Asn Gly Ala Arg Ile Arg 520

1561 TTG GCC CCA CAG AAC GAG TGG CAG GGC AAC GAG CCG GAG CGC CTG GCG AAA GTG CTG AGC 1620
521 Leu Ala Pro Gln Asn Glu Trp Gln Gly Asn Glu Pro Glu Arg Leu Ala Lys Val Leu Ser 540

1621 GTC TAC GAG CAG ATC TCT GCC GAC ACC GGC GCT AGC ATC GCG GAC GTG ATC GTT CTG GCC 1680
541 Val Tyr Glu Gln Ile Ser Ala Asp Thr Gly Ala Ser Ile Ala Asp Val Ile Val Leu Ala 560

1681 GGT AGC GTA GGC ATC GAG AAA GCC GCG AAA GCA GCA GGT TAC GAT GTG CGC GTT CCC TTC 1740
561 Gly Ser Val Gly Ile Glu Lys Ala Ala Lys Ala Ala Gly Tyr Asp Val Arg Val Pro Phe 580

1741 CTG AAA GGC CGT GGC GAT GCG ACC GCC GAG ATG ACC GAC GCA GAC TCC TTC GCA CCG CTG 1800
581 Leu Lys Gly Arg Gly Asp Ala Thr Ala Glu Met Thr Asp Ala Asp Ser Phe Ala Pro Leu 600

1801 GAG CCG CTG GCC GAT GGC TTC CGC AAC TGG CAG AAG AAA GAG TAT GTG GTG AAG CCG GAA 1860
601 Glu Pro Leu Ala Asp Gly Phe Arg Asn Trp Gln Lys Lys Glu Tyr Val Val Lys Pro Glu 620

1861 GAG ATG CTG CTG GAT CGT GCG CAG CTG ATG GGC TTA ACC GGC CCG GAA ATG ACC GTG CTG 1920
621 Glu Met Leu Leu Asp Arg Ala Gln Leu Met Gly Leu Thr Gly Pro Glu Met Thr Val Leu 640

1921 CTG GGC GGT ATG CGC GTA CTG GGC ACC AAC TAT GGT GGC ACC AAA CAC GGC GTA TTC ACC 1980
641 Leu Gly Gly Met Arg Val Leu Gly Thr Asn Tyr Gly Gly Thr Lys His Gly Val Phe Thr 660

1981 GAT TGT GAA GGC CAG TTG ACC AAC GAC TTT TTT GTG AAC CTG ACC GAT ATG GGG AAC AGC 2040
661 Asp Cys Glu Gly Gln Leu Thr Asn Asp Phe Phe Val Asn Leu Thr Asp Met Gly Asn Ser 680

2041 TGG AAG CCG GTA GGT AGC AAC GCC TAC GAA ATC CGC GAC CGC AAG ACC GGT GCC GTG AAG 2100
681 Trp Lys Pro Val Gly Ser Asn Ala Tyr Glu Ile Arg Asp Arg Lys Thr Gly Ala Val Lys 700

2101 TGG ACC GCC TCG CGG GTG GAT CTG GTA TTT GGT TCC AAC TCG CTA CTG CGC TCT TAC GCA 2160
701 Trp Thr Ala Ser Arg Val Asp Leu Val Phe Gly Ser Asn Ser Leu Leu Arg Ser Tyr Ala 720

2161 GAA GTG TAC GCC CAG GAC GAT AAC GGC GAG AAG TTC GTC AGA GAC TTC GTC GCC GCC TGG 2220
721 Glu Val Tyr Ala Gln Asp Asp Asn Gly Glu Lys Phe Val Arg Asp Phe Val Ala Ala Trp 740

2221 ACC AAA GTG ATG AAC GCC GAC CGT TTC GAC GTC GCG TCG TAA 2262
741 Thr Lys Val Met Asn Ala Asp Arg Phe Asp Val Ala Ser End 754

FIGURE 2

Microscilla furvescens Catalase 53CA1

1 ATG GAA AAT CAC AAA CAC TCA GGA TCT TCT ACG TAT AAC ACA AAC ACT GGC GGA AAA TGC 60
1 Met Glu Asn His Lys His Ser Gly Ser Ser Thr Tyr Asn Thr Asn Thr Gly Gly Lys Cys 20

61 CCT TTT ACC GGA GGT TCG CTT AAG CAA AGT GCA GGT GGC GGC ACC AAA AAC AGG GAT TGG 120
21 Pro Phe Thr Gly Gly Ser Leu Lys Gln Ser Ala Gly Gly Gly Thr Lys Asn Arg Asp Trp 40

121 TGG CCC AAC ATG CTC AAC CTC GGC ATC TTA CGC CAA CAT TCA TCG CTA TCG GAC CCA AAC 180
41 Trp Pro Asn Met Leu Asn Leu Gly Ile Leu Arg Gln His Ser Ser Leu Ser Asp Pro Asn 60

181 GAC CCG GAT TTT GAC TAT GCC GAA GAG TTT AAG AAG CTA GAT CTG GCA GCG GTT AAA AAG 240
61 Asp Pro Asp Phe Asp Tyr Ala Glu Glu Phe Lys Lys Leu Asp Leu Ala Ala Val Lys Lys 80

241 GAC CTG GCA GCG CTA ATG ACA GAT TCA CAG GAC TGG TGG CCA GCA GAT TAC GGT CAT TAT 300
81 Asp Leu Ala Ala Leu Met Thr Asp Ser Gln Asp Trp Trp Pro Ala Asp Tyr Gly His Tyr 100

301 GGC CCC TTC TTT ATA CGC ATG GCG TGG CAC AGC GCC GGC ACC TAC CGT ATC GGT GAT GGC 360
101 Gly Pro Phe Phe Ile Arg Met Ala Trp His Ser Ala Gly Thr Tyr Arg Ile Gly Asp Gly 120

361 CGT GGT GGC GGT GGC TCC GGC TCA CAG CGC TTC GCG CCT CTC AAT AGC TGG CCA GAC AAT 420
121 Arg Gly Gly Gly Gly Ser Gly Ser Gln Arg Phe Ala Pro Leu Asn Ser Trp Pro Asp Asn 140

421 GCC AAT CTG GAT AAA GCA CGC TTG CTT CTT TGG CCC ATC AAA CAA AAA TAC GGT CGA AAA 480
141 Ala Asn Leu Asp Lys Ala Arg Leu Leu Leu Trp Pro Ile Lys Gln Lys Tyr Gly Arg Lys 160

481 ATC TCC TGG GCG GAT CTA ATG ATA CTC ACA GGA AAC GTA GCT CTG GAA ACT ATG GGC TTT 540
161 Ile Ser Trp Ala Asp Leu Met Ile Leu Thr Gly Asn Val Ala Leu Glu Thr Met Gly Phe 180

541 AAA ACT TTT GGT TTT GCA GGT GGC AGA GCA GAT GTA TGG GAG CCT GAA GAA GAT GTA TAC 600
181 Lys Thr Phe Gly Phe Ala Gly Gly Arg Ala Asp Val Trp Glu Pro Glu Glu Asp Val Tyr 200

601 TGG GGA GCA GAA ACC GAA TGG CTG GGA GAC AAG CGC TAT GAA GGT GAC CGA GAG CTC GAA 660
201 Trp Gly Ala Glu Thr Glu Trp Leu Gly Asp Lys Arg Tyr Glu Gly Asp Arg Glu Leu Glu 220

661 AAT CCC CTG GGA GCC GTA CAA ATG GGA CTC ATC TAT GTA AAC CCC GAA GGA CCC AAC GGC 720
221 Asn Pro Leu Gly Ala Val Gln Met Gly Leu Ile Tyr Val Asn Pro Glu Gly Pro Asn Gly 240

721 AAG CCA GAC CCT ATC GCT GCT GCG CGT GAT ATT CGT GAG ACT TTT GGC CGA ATG GCA ATG 780
241 Lys Pro Asp Pro Ile Ala Ala Ala Arg Asp Ile Arg Glu Thr Phe Gly Arg Met Ala Met 260

781 AAT GAC GAA GAA ACC GTG GCT CTC ATA GCG GGT GGA CAC ACC TTC GGA AAA ACC CAT GGT 840
261 Asn Asp Glu Glu Thr Val Ala Leu Ile Ala Gly Gly His Thr Phe Gly Lys Thr His Gly 280

841 GCT GCC GAT GCG GAG AAA TAT GTG GGC CGA GAG CCT GCC GCC GCA GGT ATT GAA GAA ATG 900
281 Ala Ala Asp Ala Glu Lys Tyr Val Gly Arg Glu Pro Ala Ala Ala Gly Ile Glu Glu Met 300

901 AGC CTG GGG TGG AAA AAC ACC TAC GGC ACC GGA CAC GGT GCG GAT ACC ATC ACC AGT GGA 960
301 Ser Leu Gly Trp Lys Asn Thr Tyr Gly Thr Gly His Gly Ala Asp Thr Ile Thr Ser Gly 320

961 CTA GAA GGC GCC TGG ACC AAG ACC CCT ACT CAA TGG AGC AAT AAC TTT TTT GAA AAC CTC 1020
321 Leu Glu Gly Ala Trp Thr Lys Thr Pro Thr Gln Trp Ser Asn Asn Phe Phe Glu Asn Leu 340

1021 TTT GGT TAC GAG TGG GAG CTT ACC AAA AGT CCA GCT GGA GCT TAT CAG TGG AAA CCA AAA 1080
341 Phe Gly Tyr Glu Trp Glu Leu Thr Lys Ser Pro Ala Gly Ala Tyr Gln Trp Lys Pro Lys 360

1081 GAC GGT GCC GGG GCT GGC ACC ATA CCG GAT GCA CAT GAT CCC AGC AAG TCG CAC GCT CCA 1140
361 Asp Gly Ala Gly Ala Gly Thr Ile Pro Asp Ala His Asp Pro Ser Lys Ser His Ala Pro 380

1141 TTT ATG CTC ACT ACG GAC CTG GCG CTG CGC ATG GAC CCT GAT TAC GAA AAA ATT TCT CGA 1200
381 Phe Met Leu Thr Thr Asp Leu Ala Leu Arg Met Asp Pro Asp Tyr Glu Lys Ile Ser Arg 400

1201 CGG TAC TAT GAA AAC CCT GAT GAG TTT GCA GAT GCT TTC GCG AAA GCA TGG TAC AAA CTG 1260
401 Arg Tyr Tyr Glu Asn Pro Asp Glu Phe Ala Asp Ala Phe Ala Lys Ala Trp Tyr Lys Leu 420

1261 ACA CAC AGA GAT ATG GGA CCA AAG GTG CGC TAC CTG GGA CCA GAA GTG CCT CAG GAA GAC 1320
421 Thr His Arg Asp Met Gly Pro Lys Val Arg Tyr Leu Gly Pro Glu Val Pro Gln Glu Asp 440

1321 CTC ATC TGG CAA GAC CCT ATA CCA GAT GTA AGC CAT CCT CTT GTA GAC GAA AAC GAT ATT 1380
441 Leu Ile Trp Gln Asp Pro Ile Pro Asp Val Ser His Pro Leu Val Asp Glu Asn Asp Ile 460

1381 GAA GGC CTA AAA GCC AAA ATC CTG GAA TCG GGA CTG ACG GTA AGC GAG CTG GTA AGC ACG 1440
461 Glu Gly Leu Lys Ala Lys Ile Leu Glu Ser Gly Leu Thr Val Ser Glu Leu Val Ser Thr 480

1441 GCA TGG GCT TCT GCA TCT ACT TTT AGA AAC TCT GAC AAG CGC GGC GGT GCC AAC GGT GCA 1500
481 Ala Trp Ala Ser Ala Ser Thr Phe Arg Asn Ser Asp Lys Arg Gly Gly Ala Asn Gly Ala 500

1501 CGT ATA CGA CTG GCC CCA CAA AAA GAC TGG GAA GTA AAC AAC CCT CAG CAA CTT GCC AGG 1560
501 Arg Ile Arg Leu Ala Pro Gln Lys Asp Trp Glu Val Asn Asn Pro Gln Gln Leu Ala Arg 520

1561 GTA CTC AAA ACA CTA GAA GGT ATC CAG GAG GAC TTT AAC CAG GCG CAA TCA GAT AAC AAA 1620
521 Val Leu Lys Thr Leu Glu Gly Ile Gln Glu Asp Phe Asn Gln Ala Gln Ser Asp Asn Lys 540

1621 GCA GTA TCG TTG GCC GAC CTG ATT GTG CTG GCC GGC TGT GCG GGT GTA GAA AAA GCT GCA 1680
541 Ala Val Ser Leu Ala Asp Leu Ile Val Leu Ala Gly Cys Ala Gly Val Glu Lys Ala Ala 560

1681 AAA GAT GCT GGC CAT GAG GTG CAG GTG CCT TTC AAC CCG GGA CGA GCG GAT GCC ACC GCT 1740
561 Lys Asp Ala Gly His Glu Val Gln Val Pro Phe Asn Pro Gly Arg Ala Asp Ala Thr Ala 580

1741 GAG CAA ACC GAT GTG GAA GCT TTC GAA GCA CTA GAG CCA GCG GCT GAC GGC TTT AGA AAC 1800
581 Glu Gln Thr Asp Val Glu Ala Phe Glu Ala Leu Glu Pro Ala Ala Asp Gly Phe Arg Asn 600

1801 TAC ATT AAA CCG GAG CAT AAA GTA TCC GCT GAG GAA ATG CTC GTA GAC CGG GCG CAG CTT 1860
601 Tyr Ile Lys Pro Glu His Lys Val Ser Ala Glu Glu Met Leu Val Asp Arg Ala Gln Leu 620

1861 CTG TCG CTT TCG GCA CCA GAA ATG ACT GCT TTG GTA GGC GGT ATG CGT GTA CTG GGC ACC 1920
621 Leu Ser Leu Ser Ala Pro Glu Met Thr Ala Leu Val Gly Gly Met Arg Val Leu Gly Thr 640

1921 AAC TAC GAC GGT TCG CAG CAT GGA GTG TTT ACA AAT AAG CCG GGT CAG CTA TCC AAT GAC 1980
641 Asn Tyr Asp Gly Ser Gln His Gly Val Phe Thr Asn Lys Pro Gly Gln Leu Ser Asn Asp 660

1981 TTC TTT GTA AAC CTG CTA GAC CTC AAC ACT AAA TGG CGA GCC AGC GAT GAA TCA GAC AAA 2040
661 Phe Phe Val Asn Leu Leu Asp Leu Asn Thr Lys Trp Arg Ala Ser Asp Glu Ser Asp Lys 680

2041 GTT TTT GAA GGC AGA GAC TTC AAA ACT GGC GAA GTA AAG TGG AGT GGC ACC CGG GTA GAC 2100
681 Val Phe Glu Gly Arg Asp Phe Lys Thr Gly Glu Val Lys Trp Ser Gly Thr Arg Val Asp 700

2101 CTG ATC TTC GGA TCC AAT TCC GAG CTA AGA GCC CTC GCA GAA GTG TAC GGC TGT GCA GAT 2160
701 Leu Ile Phe Gly Ser Asn Ser Glu Leu Arg Ala Leu Ala Glu Val Tyr Gly Cys Ala Asp 720

2161 TCT GAA GAA AAG TTT GTT AAA GAT TTT GTG AAG GCC TGG GCC AAA GTA ATG GAC CTG GAC 2220
721 Ser Glu Glu Lys Phe Val Lys Asp Phe Val Lys Ala Trp Ala Lys Val Met Asp Leu Asp 740

2221 CGG TTT GAT CTG AAA TAA 2238
741 Arg Phe Asp Leu Lys End 746

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/16513

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12N 9/08, 15/53, 15/63, 1/21, 15/09; C12P 1/00; C12Q 1/30
US CL :435/192, 320.1, 252.3, 41, 27; 536/23.2
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/192, 320.1, 252.3, 41, 27; 536/23.2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- A	FORKL H. et al. Molecular Cloning, Sequence Analysis and Expression of the Gene for Catalase-Peroxidase (*cpeA*) From the Photosynthetic Bacterium *Rhodobacter capsulatus* B10. Eur. J. Biochem. 1993, Vol. 214, pages 251-258, see Figure 4.	3, 13 ------- 1, 2, 4-9, 14-17
X --- A	LOPRASERT, S. et al. Cloning, Nucleotide Sequence, and Expression in *Escherichia coli* of the *Bacillus stearothermophilus* Peroxidase Gene (*perA*). J. Bacteriol. September 1989, Vol. 171, No. 9, pages 4871-4875, see Figure 2.	3, 13 -------- 1, 2, 4-9, 14-17

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 OCTOBER 1997	31 OCT 1997

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/16513

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

APS, MEDLINE, SCISEARCH, LIFESCI, EMBASE, WPI, CAS, NTIS, BIOTECHDS, BIOSIS
search terms: catalase#, acaligenes or delaya or aquamarinus, microscilla or furvescens

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-9 and 13-17, drawn to catalases, method of making and method of use thereof.
Group II, claims 10-12, drawn to catalase antibodies.

The inventions listed as Groups I and II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the proteins of Groups I and II are structurally unrelated amino acid sequences.